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DynaGeV

Dynamique des Génomes Végétaux

Workshop on Plant Genome Dynamics and Evolution

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diversity, organization and dynamics

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INVESTISSEMENTS D'AVENIR

Using the 3k genomes to decipher the mosaic structure of genome diversity in rice

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Introgression among rice populations is worth studying for its role as a path to adaptation. Along human migrations, gene flow between cultivars and wild or primitive cultivated forms have generated new types which thus harbor admixed genomes with distinct components traceable to early crop history. Recent analyses based on massive sequencing efforts have enabled detailed studies of crop evolution in rice that revealed introgressions allowing the spread of domestication factors across varietal groups as well as the secondary hybrid origin of some varietal clusters. Yet distinct views still coexist as to the global interpretation of the data, featuring one *vs* multiple domestication events and diverse scenarios for the origin of secondary varietal groups. Contrasting hypotheses make it difficult to draw conclusions from the data given their weight on the premises underlying any analysis. Nonetheless, by recognizing the existence of more or less cohesive groups of rice varieties, important information can still be extracted as to their interactions. The results presented here are a still frame of our analysis of the exchanges between the major clusters of rice genetic diversity, Japonica, Indica and *circum*Aus, as can be determined by their relative differentiation, and the concomitant retrieval of the cryptic *circum*Basmati genetic signature.

Keywords: *rice, gene flow, admixed genomes, cBasmati, mosaic*

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